

SEQUENCE LISTING

<110> Allen, Keith D.
Matthews, William
Moore, Mark

<120> TRANSGENIC MICE CONTAINING GLUCAGON
RECEPTOR GENE DISRUPTIONS

<130> R-648

<140> To Be Assigned

<141> Herewith

<150> US 60/251,804

<151> 2000-12-06

<150> US 60/266,044

<151> 2001-02-01

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1944

<212> DNA

<213> Mus musculus

<400> 1

```
cagggtctcc cttgcaacct gaggagaggt gcacacactc tgaggaccta ggtgtgcaac 60
ctctgccaga tgtggggcgt ggctaccacag aggcattgcc ctcaccacag tccactgtcc 120
ccacctgctg ctgctgctgt tgggtgctgtc atgtctgcca gaggcaccct ctgcccaggt 180
aatggacttt ttgtttgaga agtgggaagct ctatagtac caatgtcacc acaacctaaag 240
cctgctgccc ccacctactg agctgggtctg taacagaacc ttcgacaact actcctgctg 300
gcctgacacc cctcccaaca ccactgccaa catttcctgc ccctgggtacc taccttggtg 360
ccacaaagtg cagcaccgcc tagtggtcaa gaggtgtggg cccgatgggc agtgggttcg 420
agggccacgg gggcagccgt ggcgcaacgc ctcccaatgt cagttggatg atgaagagat 480
cgaggtccag aaggggggtg ccaagatgta tagcagccag caggtgatgt acaccgtggg 540
ctacagtctg tccctggggg ccttgctcct tgcgctggtc atcctgctgg gcctcaggaa 600
gctgcactgc acccgaaact acatccatgg gaacctgttt gcgtcctttg tgctcaaggc 660
tggtctctgt ttggtcatcg attggctgct gaagacacgg tacagccaga agattggcga 720
tgacctcagt gtgagcgtct ggctcagtga cggggcgatg gccggctgca gagtggccac 780
agtgatcatg cagtacggca tcatacccaa ctattgctgg ttgctggtag agggcggtga 840
cctgtacagc ctgctgagcc ttgccacct ctctgagagg agcttctttt ccctctacct 900
gggcattggc tgggggtgct ccctgctgtt tgtcatcccc tgggtgggtg tcaagtgtct 960
gtttgagaat gttcagtgt ggaccagcaa tgacaacatg ggattctggt ggatcctgct 1020
tattcctgtc ttctggcct tactgatcaa ttttttcac tttgtccaca tcattcaact 1080
tcttgtggcc aagctgctg cccatcagat gcactatgct gattacaagt tccggctggc 1140
caggtccacg ctgacctca tccctctgct ggggggtccac gaggtgggtc ttgcctttgt 1200
gactgacgag catgcccaag gcaccctgct ctccaccaag ctcttttttg acctgttct 1260
cagctccttc caggggtctg tgggtggctgt tctctactgt ttcctcaaca aggaggtgca 1320
ggcagagctg atgcccgtt ggaggcaatg gcaagaaggc aaagctcttc aggaggaaag 1380
gttgccagc agccatggca gccacatggc cccagcaggc ccttgctcat gtgatccctg 1440
tgagaaactt cagcttatga gtgcaggcag cagcagtggg actggctgtg tgccctctat 1500
ggagacctcg ctggccagta gtctcccaag gttggctgac agccccacct gaatctccac 1560
ttggagccta ggcaggttgt gttcaagaaa gggcctcaga ggacaacca gagccagatg 1620
cccggccaag gttgaagagc caaagcagca agacagcagc ttgtactgtg cacactcccc 1680
taacctgtcc tagcctggca caggccacag tgacagagta ggggttggat atgatggaga 1740
```

agccatgtta tctatgaact ctgagtgttc ccatgtgtgt tgacatgggc cctgtaccca 1800
gatatgtcct tcagtaaaaa gctcgagtgg agctgctgca cagctcgtgg acagcaggct 1860
tgaagcccc agggacgggg ttggggaggc cggggatgag cagcacactc agcagggtga 1920
gcgctagtgc aaccaggaa agaa 1944

<210> 2
<211> 485
<212> PRT
<213> Mus musculus

<400> 2
Met Pro Leu Thr Gln Leu His Cys Pro His Leu Leu Leu Leu Leu Leu
1 5 10 15
Val Leu Ser Cys Leu Pro Glu Ala Pro Ser Ala Gln Val Met Asp Phe
20 25 30
Leu Phe Glu Lys Trp Lys Leu Tyr Ser Asp Gln Cys His His Asn Leu
35 40 45
Ser Leu Leu Pro Pro Pro Thr Glu Leu Val Cys Asn Arg Thr Phe Asp
50 55 60
Asn Tyr Ser Cys Trp Pro Asp Thr Pro Pro Asn Thr Thr Ala Asn Ile
65 70 75 80
Ser Cys Pro Trp Tyr Leu Pro Trp Cys His Lys Val Gln His Arg Leu
85 90 95
Val Phe Lys Arg Cys Gly Pro Asp Gly Gln Trp Val Arg Gly Pro Arg
100 105 110
Gly Gln Pro Trp Arg Asn Ala Ser Gln Cys Gln Leu Asp Asp Glu Glu
115 120 125
Ile Glu Val Gln Lys Gly Val Ala Lys Met Tyr Ser Ser Gln Gln Val
130 135 140
Met Tyr Thr Val Gly Tyr Ser Leu Ser Leu Gly Ala Leu Leu Leu Ala
145 150 155 160
Leu Val Ile Leu Leu Gly Leu Arg Lys Leu His Cys Thr Arg Asn Tyr
165 170 175
Ile His Gly Asn Leu Phe Ala Ser Phe Val Leu Lys Ala Gly Ser Val
180 185 190
Leu Val Ile Asp Trp Leu Leu Lys Thr Arg Tyr Ser Gln Lys Ile Gly
195 200 205
Asp Asp Leu Ser Val Ser Val Trp Leu Ser Asp Gly Ala Met Ala Gly
210 215 220
Cys Arg Val Ala Thr Val Ile Met Gln Tyr Gly Ile Ile Pro Asn Tyr
225 230 235 240
Cys Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Ser Leu Leu Ser Leu
245 250 255
Ala Thr Phe Ser Glu Arg Ser Phe Phe Ser Leu Tyr Leu Gly Ile Gly
260 265 270
Trp Gly Ala Pro Leu Leu Phe Val Ile Pro Trp Val Val Lys Cys
275 280 285
Leu Phe Glu Asn Val Gln Cys Trp Thr Ser Asn Asp Asn Met Gly Phe
290 295 300
Trp Trp Ile Leu Arg Ile Pro Val Phe Leu Ala Leu Leu Ile Asn Phe
305 310 315 320
Phe Ile Phe Val His Ile Ile Gln Leu Leu Val Ala Lys Leu Arg Ala
325 330 335
His Gln Met His Tyr Ala Asp Tyr Lys Phe Arg Leu Ala Arg Ser Thr
340 345 350
Leu Thr Leu Ile Pro Leu Leu Gly Val His Glu Val Val Phe Ala Phe
355 360 365
Val Thr Asp Glu His Ala Gln Gly Thr Leu Arg Ser Thr Lys Leu Phe
370 375 380
Phe Asp Leu Phe Leu Ser Ser Phe Gln Gly Leu Leu Val Ala Val Leu
385 390 395 400

